



102790-135 sequence listing

SEQUENCE LISTING

<110> Givaudan SA

<120> G-Proteins

<130> 30069PCT

<150> US 60/434,790

<151> 2002-12-18

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1122

<212> DNA

<213> Homo sapiens

<221> CDS

<222> (1)..(1122)

<400> 1

```
atgccccgct cgctgacctg gcgctgctgc ccctggtgcc tgacggagga tgagaaggcc 60
gccgcccggg tggaccagga gatcaacagg atcctcttgg agcagaagaa gcaggaccgc 120
ggggagctga agctgctgct tttggggcca ggcgagagcg ggaagagcac cttcatcaag 180
cagatgcgga tcatccacgg cgccggctac tcggaggagg agcgcaaggg cttccggccc 240
ctggtctacc agaacatctt cgtgtccatg cgggccatga tcgaggccat ggagcggctg 300
cagattccat tcagcaggcc cgagagcaag caccacgcta gcctgggtcat gagccaggac 360
ccctataaag tgaccacgtt tgagaagcgc tacgctgcgg ccatgcagtg gctgtggagg 420
gatgccggca tccgggcctg ctatgagcgt cggcgggaat tccacctgct cgattcagcc 480
gtgtactacc tgtcccacct ggagcgcata accgaggagg gctacgtccc cacagctcag 540
gacgtgctcc gcagccgcat gcccaccact ggcatcaacg agtactgctt ctccgtgcag 600
aaaaccaacc tgcggatcgt ggacgtcggg ggccagaagt cagagcgtaa gaaatggatc 660
cattgtttcg agaacgtgat cgccctcatc tacctggcct cactgagtga atacgaccag 720
tgcttgaggg agaacaacca ggagaaccgc atgaaggaga gcctcgattt gtttgggact 780
atcctggaac taccctggtt caaaagcaca tccgtcatcc tctttctcaa caaaaccgac 840
atcctggagg agaaaatccc cacctcccac ctggctacat atttccccag tttccagggc 900
cctaagcagg atgctgaggc agccaagagg ttcacatcctgg acatgtacac gaggatgtac 960
```

102790-135 sequence listing

accgggtgcg tggacggccc cgagggcagc aacttaaaaa aagaagataa ggaaatctat 1020
tctcacatga cctgcgctac tgacacacaa aacgtcaaat tcgtgtttga tgccgtgaca 1080
gatataataa taaaagagaa cctcaaagac tgtgggctct tc 1122

<210> 2

<211> 374

<212> PRT

<213> Homo sapiens

<400> 2

Met	Ala	Arg	Ser	Leu	Thr	Trp	Arg	Cys	Cys	Pro	Trp	Cys	Leu	Thr	Glu
1				5					10					15	
Asp	Glu	Lys	Ala	Ala	Ala	Arg	Val	Asp	Gln	Glu	Ile	Asn	Arg	Ile	Leu
			20					25					30		
Leu	Glu	Gln	Lys	Lys	Gln	Asp	Arg	Gly	Glu	Leu	Lys	Leu	Leu	Leu	Leu
		35					40					45			
Gly	Pro	Gly	Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile
	50					55					60				
Ile	His	Gly	Ala	Gly	Tyr	Ser	Glu	Glu	Glu	Arg	Lys	Gly	Phe	Arg	Pro
65					70					75					80
Leu	Val	Tyr	Gln	Asn	Ile	Phe	Val	Ser	Met	Arg	Ala	Met	Ile	Glu	Ala
				85					90					95	
Met	Glu	Arg	Leu	Gln	Ile	Pro	Phe	Ser	Arg	Pro	Glu	Ser	Lys	His	His
			100					105					110		
Ala	Ser	Leu	Val	Met	Ser	Gln	Asp	Pro	Tyr	Lys	Val	Thr	Thr	Phe	Glu
		115					120					125			
Lys	Arg	Tyr	Ala	Ala	Ala	Met	Gln	Trp	Leu	Trp	Arg	Asp	Ala	Gly	Ile
	130					135					140				
Arg	Ala	Cys	Tyr	Glu	Arg	Arg	Arg	Glu	Phe	His	Leu	Leu	Asp	Ser	Ala
145					150					155					160
Val	Tyr	Tyr	Leu	Ser	His	Leu	Glu	Arg	Ile	Thr	Glu	Glu	Gly	Tyr	Val
				165					170					175	
Pro	Thr	Ala	Gln	Asp	Val	Leu	Arg	Ser	Arg	Met	Pro	Thr	Thr	Gly	Ile
			180					185					190		
Asn	Glu	Tyr	Cys	Phe	Ser	Val	Gln	Lys	Thr	Asn	Leu	Arg	Ile	Val	Asp
		195					200					205			
Val	Gly	Gly	Gln	Lys	Ser	Glu	Arg	Lys	Lys	Trp	Ile	His	Cys	Phe	Glu
	210					215					220				
Asn	Val	Ile	Ala	Leu	Ile	Tyr	Leu	Ala	Ser	Leu	Ser	Glu	Tyr	Asp	Gln
225					230					235					240

102790-135 sequence listing

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
245 250 255

Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
260 265 270

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
290 295 300

Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
305 310 315 320

Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Leu Lys Lys Glu Asp
325 330 335

Lys Glu Ile Tyr Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val
340 345 350

Lys Phe Val Phe Asp Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu
355 360 365

Lys Asp Cys Gly Leu Phe
370